AMENDMENT TO THE SPECIFICATION

Please replace the paragraph beginning on page 11, line 23 and ending on page 12, line 3, with the following paragraph:

Figure 4 illustrates SNP detection of the factor V gene (1691 G ->A) with unamplified human genomic DNA [part (a)] or salmon sperm DNA [part (b)] on ~~Superaldehyde®~~SUPERALDEHYDE® slides that have wild type or mutant factor V gene capture probes. Part (c) is a graph that summarizes a detection signal intensity analysis for human genomic DNA and nonspecific salmon sperm DNA in the presence of either the wild type or mutant capture probes.

Please replace the paragraph on page 12, lines 11-17, with the following paragraph:

Figure 7 demonstrates SNP detection of the factor V mutant gene (1691 G ->A) with unamplified human genomic DNA (part (a)) using hybridizations with various formamide concentrations on CODELINK®~~CodeLink®~~ slides that have arrayed wild-type and mutant factor V gene capture probes. Part (b) is a graph that summarizes the detection signal intensity analysis for human genomic DNA following hybridizations with various formamide concentrations in the presence of either the wild-type or mutant capture probes.

Please replace the paragraph beginning on page 15, line 20 and ending on page 16, line 2, with the following paragraph:

Figure 21 is a graph that illustrates the sensitivity limit for mecA gene detection using a genomic DNA target. Data analysis of mecA gene detection in a genomic sample of ATCC 700699 using the sequences from Table 3 in 5x SCC, 0.05% TWEEN 20~~Tween 20~~, 0.01% BSA, 15% v/v formamide and 200 pM nanoparticle probe at 45C for 1.5 hours. The graph shows a limit of detection at 330 fM in a 50 µl reaction (34 ng total genomic DNA). Three standard deviations over the background is represented by the horizontal at 80 in the plot.

Please replace the paragraph on page 42, lines 2-8, with the following paragraph:

Capture strands were arrayed on SUPERALDEHYDE®~~Superaldehyde~~ slides (Telechem)

or CODELINK® ~~CodeLinke~~ slides (Amersham, Inc.) by using a GMS417 arrayer (Affymetrix). The positioning of the arrayed spots was designed to allow multiple hybridization experiments on each slide, achieved by partitioning the slide into separate test wells by silicone gaskets (Grace Biolabs). The wild type and mutant spots were spotted in triplicate in manufacturer-provided spotting buffers. Protocols recommended by the manufacturer were followed for post-array processing of the slides.

Please replace the paragraph on page 42, lines 12-25, with the following paragraph:

The Factor V SNP detection was performed by employing the following protocol. Sonicated human placental DNA, genotyped as homozygous wild-type, or salmon sperm DNA (Sigma) was precipitated with ethanol and dissolved in a 10 nM solution of FV probe solution. Additional components were added to this mixture such that the final hybridization mixture (5 μL) contained 3×SSC, 0.03% TWEEN 20 ~~Tween 20~~, 23% formamide, 5 nM FV probe, and 10 μg human DNA, or as indicated. The hybridization mixture was added to the test well after a 4 min, 99 °C heat denaturation step. The arrays were incubated at 50°C for 90 min. Post-hybridization washes were initiated by immersing arrays for 1 min in 0.5 M $NaNO_3$, 0.05% TWEEN 20 ~~Tween 20~~ at room temperature. The gasket was removed and the test slide was washed again in 0.5M $NaNO_3$/0.05% TWEEN 20 ~~Tween 20~~ solution and incubated at room temperature for 3 min (2×) with gentle agitation. The slides were stained with the silver enhancing solution as described above and dried on a spin dryer and imaged on an ARRAYWORX® ~~ArrayWorx®~~ biochip reader (Model no. AWE, Applied Precision Inc., Issaquah, WA, U.S.A.).

Please replace the paragraph on page 43, lines 3-12, with the following paragraph:

Figure 4 shows SNP discrimination of Factor V gene in human genomic DNA on Superaldehyde slides. The test array contains wild type and mutant capture spots. The array shown on the top was hybridized with wild-type human genomic DNA while the array on the bottom was hybridized with sonicated salmon sperm DNA. The signal at the wild-type spots is significantly higher than mutant spots with wild-type human genomic DNA hybridization to indicate a Factor V homozygous wild-type genotype. Under the hybridization conditions, no signal is observed for the salmon sperm DNA hybridization and serves as a control in the assay. SNP discrimination was also examined with arrays on CODELINK® ~~CodeLink®~~ slides.

Please replace the paragraph on page 45, lines 7-25, with the following paragraph:

Capture oligonucleotides of various lengths, including 20, 21, 24, or 26 nucleotides (FV-WT20 (SEQ ID NO: 13): 5'(GGACAGGCGAGGAATACAGG)-(PEG)x3-NH_2, 3' FV-mut21 (SEQ ID NO: 14): 5'(TGGACAGGCAAGGAATACAGG)-(PEG)x3-NH_2 3', FV-wt24 (SEQ ID NO: 15): 5' TGG ACA GGC GAG GAA TAC AGG TAT-NH_2 3', FV-mut26 (SEQ ID NO: 16): 5' CTG GAC AGG CAA GGA ATA CAG GTA TT-NH_2 3') were printed on CODELINK®~~CodeLink~~ slides as described above and were added to 5 μg of normal human placenta genomic DNA (Sigma, St. Louis, MO) or factor V mutant human genomic DNA (isolated from repository culture GM14899, factor V deficiency, Coriell Institute). The slides and DNA were incubated in 20% FM, 30% FM, or 40% FM, and 4X SSC/0/04% TWEEN 20~~Tween~~ at 40°C for 2 hours in the first step. The slides were then washed in 2XSSC at room temperature for 3 minutes. After washing, nanoparticle probes with detection oligonucleotides that recognized Factor V were added and the mixture was then incubated for 1 hour at 40°C. The signal was detected by silver staining as described above. The results showed that under optimally tuned conditions (30% FM in this case), the human wt DNA generated a signal on the wt probes only, while the human mutant DNA generated a signal only at the mutant capture probes (Figure 8). Changing the stringency conditions resulted in either loss of discrimination (stringency too low) or loss of signal (stringency too high). Figure 9 shows the quantitative data for the perfect (center) hybridization condition in Figure 8.

Please replace the paragraph on page 53, lines 5-18, with the following paragraph:

3'-amino and 5'- amino containing DNA was synthesized by following standard protocol for DNA synthesis on DNA synthesizer. The amine modified DNA was attached to the aldehyde microarray slide by printing a 1 mM DNA solution in ArrayIt buffer plus (Catalog no.MSP, Company nameTelechem, citySunnyvale, StateCA). An AFFYMETRIX®~~Affymetrix®~~ GMS 417 arrayer (Affymetrix, city Santa Clara, state CA) with 500 micron printing pins was used to orient the microarray on the slide. The microarray slide was purchased from Telechem (catalog no. SMM, city Sunnyvale, state CA) with an aldehyde functionalized surface. After printing, the slides were placed in a humidified chamber at ambient temperature for 12-18 hrs. The slides were removed and dried under vacuum for 30 min to 2 hrs. The slides were then subjected to

two washes in 0.2 % w/v SDS and two washes in water to remove any remaining unbound DNA. The slides were then treated with a solution of 2.5 M sodium borohydride in 1X PBS with 20 % v/v 100% ethanol by soaking for 5 min. The slides were then washed three times with 0.2 % w/v SDS and twice with water and centrifuged dry.

Please replace the paragraph on page 60, lines 1-11, with the following paragraph:

Reaction mixtures of bacterial genomic DNA ranging in amount from 250 ng – 1 ug and 1nM nanoparticle probes were made in 1x hybridization buffer (5X SSC, 0.05 % TWEEN 20~~Tween 20~~). The reaction mixture was heated to 95 °C for 5 minutes. Subsequently, 10-25 ul of the reaction mixture was added to the microarray surface and hybridized at 40 °C and 90 % relative humidity for 2 hours. The microarray surface was washed for 30 sec in 5X SSC, 0.05 % TWEEN 20~~Tween 20~~ at room temperature, then washed for another 30 sec with 0.5 M $NaNO_3$ also at room temperature. The microarray was dried and exposed with silver development using commercial grade silver enhancer solutions (Silver Enhancer Kit, Catalog No. SE-100, Sigma, St. Louis) for 4 minutes. The silver stained microarray plate was then washed, dried and imaged using an ARRAYWORX®~~Arrayworx®~~ scanner (Model No. AWE, Applied Precision, Inc., Issaquah, WA).

Please replace the paragraph beginning on page 61, line 18 and ending on page 62, line 6, with the following paragraph:

In separate hybridization wells, fragmented total genomic DNA isolated from Staphylococcus epidermidis or Staphylococcus aureus bacterial cells (8.0 E07 copies, ~ 250 ng) and 1nM nanoparticle probes were mixed in 1x hybridization buffer (5X SSC, 0.05 % TWEEN 20~~Tween 20~~). As a positive control, PCR-amplifed Tuf gene fragments of the same genomic DNA samples were mixed with probes and buffer in separate hybridization wells on the glass slide. The reaction mixture was heated to 95 °C for 5 minutes. Subsequently, 50 ul of the reaction mixture was added to the microarray surface and hybridized at 45 °C and 90 % relative humidity for 1.5 hours. The microarray surface was washed for 30 sec in 0.5 M $NaNO_3$ at room temperature. The microarray was dried and exposed with silver development using commercial grade silver enhancer solutions (Silver Enhancer Kit, Catalog No. SE-100, Sigma, St. Louis, MO) for 4 minutes. The silver stained microarray plate was then washed, dried, and the light

scattered from silver amplified nanoparticle probes on the array was imaged and quantified using an ARRAYWORX®~~Arrayworx®~~ scanner (Model No. AWE, Applied Precision, Issaquah, WA).

Please replace the paragraph on page 63, lines 16-23, with the following paragraph:

Each reaction consisted of 50 ul of 5x SSC, 0.05 % TWEEN 20~~Tween 20~~, 0.01 % BSA, 200 pM each nanoparticle probe, 15 % formamide and 750 pM of each target amplicon. The reagents were hybridized for 1 hr at 40 C and 90 % humidity. The microarray surface was washed for 30 sec in 0.5 M $NaNO_3$ at room temperature. The microarray was dried and exposed with silver development using commercial grade silver enhancer solutions (Silver Enhancer Kit, Catalog No. SE-100, Sigma, St. Louis, MO) for 4 minutes. The silver stained microarray plate was then washed, dried and imaged using an ARRAYWORX®~~Arrayworx®~~ scanner (Model No. AWE, Applied Precision, Issaquah, WA).

Please replace the paragraph beginning on page 64, line 9 and ending on page 65, line 2, with the following paragraph:

In this Example, the identification of Staphylococcus genus, species, and antibiotic resistance status was tested using total genomic DNA isolated from *S. aureus* and *S. epidermidis* bacterial cells. The genomic DNA samples tested were characterized by ATCC as described in table 3 above. The microarray plates and detection probes used for testing in example 6 also were used for this example. The microarray plates and capture and detection probes were prepared as described in Example 3. The genomic DNA samples were prepared as described in example 5. Each reaction consisted of 50 ul of 5x SSC, 0.05 % TWEEN 20~~Tween 20~~, 0.01 % BSA, 200 pM each nanoparticle probe, and 15 % formamide and 3.3 ng/ul of sonicated genomic DNA. The reagents were hybridized for 2 hrs at 40 C and 90 % humidity. The microarray surface was washed for 30 sec in 0.5 M $NaNO_3$ at room temperature. The microarray was dried and exposed with silver development using commercial grade silver enhancer solutions (Silver Enhancer Kit, Catalog No. SE-100, Sigma, St. Louis) for 4 minutes. The silver stained microarray plate was then washed, dried and imaged using an ARRAYWORX®~~Arrayworx®~~ scanner (Model No. AWE, Applied Precision, Issaquah, WA).